

Amendment to the Claims:

Please amend the claims as follows.

Please cancel claims 1 to 41 and 56 to 92, without prejudice.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claims 1 to 41 (canceled)

Claim 42 (currently amended): A method of generating a variant comprising:
obtaining a nucleic acid comprising a sequence selected from the group consisting of (a) a sequence comprising SEQ ID NO:7 ~~SEQ ID NOS: 5, 7~~, (b) sequences substantially identical to SEQ ID NO:7 thereto, ~~sequences complementary thereto~~, (c) fragments comprising at least 30 consecutive nucleotides of a sequence as set forth in SEQ ID NO:7, (d) a sequence having at least about 50% sequence identity to a sequence as set forth in SEQ ID NO:7 thereof, and ~~(d) fragments comprising at least 30 consecutive nucleotides of the sequences~~ complementary to (a), (b), (c) or (d) ~~SEQ ID NOS: 5, 7~~; and
modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.

Claim 43 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis and any combination thereof.


Claim 44 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by error-prone PCR.

Claim 45 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by shuffling.

Claim 46 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

Claim 47 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by assembly PCR.

Claim 48 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by sexual PCR mutagenesis.

 Claim 49 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by *in vivo* mutagenesis.

Claim 50 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by cassette mutagenesis.

Claim 51 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by recursive ensemble mutagenesis.

Claim 52 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by exponential ensemble mutagenesis.

Claim 53 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by site-specific mutagenesis.

Claim 54 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by gene reassembly.

Claims 55 to 92 (canceled)

Claim 93 (new): A method of generating a variant comprising:

obtaining a nucleic acid comprising (a) a sequence comprising SEQ ID NO:5, (b) a sequence having at least about 65% sequence identity to SEQ ID NO:5, (c) fragments comprising at least about 30 consecutive nucleotides of a sequence as set forth in SEQ ID NO:5 or a sequence having at least about 65% sequence identity to SEQ ID NO:5, or (d) a sequence to (a), (b), (c) or (d); and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.

Claim 94 (new): A method of generating a variant catalase comprising:

obtaining a nucleic acid comprising a sequence as set forth in SEQ ID NO:5 or SEQ ID NO:7; and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence, thereby generating a variant catalase.

Claim 95 (new): The method of claim 42, wherein the sequence has at least about 55% sequence identity to SEQ ID NO:7.

Claim 96 (new): The method of claim 95, wherein the sequence has at least about 60% sequence identity to SEQ ID NO:7.

Claim 97 (new): The method of claim 96, wherein the sequence has at least about 65% sequence identity to SEQ ID NO:7.

Claim 98 (new): The method of claim 97, wherein the sequence has at least about 70% sequence identity to SEQ ID NO:7.

Claim 99 (new): The method of claim 98, wherein the sequence has at least about 75% sequence identity to SEQ ID NO:7.

Claim 100 (new): The method of claim 99, wherein the sequence has at least about 80% sequence identity to SEQ ID NO:7.

Claim 101 (new): The method of claim 100, wherein the sequence has at least about 85% sequence identity to SEQ ID NO:7.

Claim 102 (new): The method of claim 101, wherein the sequence has at least about 90% sequence identity to SEQ ID NO:7.

Claim 103 (new): The method of claim 102, wherein the sequence has at least about 95% sequence identity to SEQ ID NO:7.

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Claim 104 (new): The method of claim 103, wherein the sequence has at least about 96% sequence identity to SEQ ID NO:7.

Claim 105 (new): The method of claim 104, wherein the sequence has at least about 97% sequence identity to SEQ ID NO:7.

Claim 106 (new): The method of claim 105, wherein the sequence has at least about 98% sequence identity to SEQ ID NO:7.

Claim 107 (new): The method of claim 106, wherein the sequence has at least about 99% sequence identity to SEQ ID NO:7.

Claim 108 (new): The method of claim 97, wherein the sequence has at least about 70% sequence identity to SEQ ID NO:5.


Claim 109 (new): The method of claim 108, wherein the sequence has at least about 75% sequence identity to SEQ ID NO:5.

Claim 110 (new): The method of claim 109, wherein the sequence has at least about 80% sequence identity to SEQ ID NO:5.

Claim 111 (new): The method of claim 110, wherein the sequence has at least about 85% sequence identity to SEQ ID NO:5.

Claim 112 (new): The method of claim 111, wherein the sequence has at least about 90% sequence identity to SEQ ID NO:5.

Claim 113 (new): The method of claim 112, wherein the sequence has at least about 95% sequence identity to SEQ ID NO:5.

 Claim 114 (new): The method of claim 113, wherein the sequence has at least about 96% sequence identity to SEQ ID NO:5.

Claim 115 (new): The method of claim 114, wherein the sequence has at least about 97% sequence identity to SEQ ID NO:5.

Claim 116 (new): The method of claim 115, wherein the sequence has at least about 98% sequence identity to SEQ ID NO:5.

Claim 117 (new): The method of claim 116, wherein the sequence has at least about 99% sequence identity to SEQ ID NO:5.
